The chicken talpid\textsuperscript{3} gene encodes a novel protein essential for Hedgehog signaling

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\textbf{Talpid}\textsuperscript{3} is a classical chicken mutant with abnormal limb patterning and malformations in other regions of the embryo known to depend on Hedgehog signaling. We combined the ease of manipulating chicken embryos with emerging knowledge of the chicken genome to reveal directly the basis of defective Hedgehog signal transduction in talpid\textsuperscript{3} embryos and to identify the talpid\textsuperscript{3} gene. We show in several regions of the embryo that the talpid\textsuperscript{3} phenotype is completely ligand independent and demonstrate for the first time that talpid\textsuperscript{3} is absolutely required for the function of both Gli repressor and activator in the intracellular Hedgehog pathway. We map the talpid\textsuperscript{3} locus to chromosome 5 and find a frameshift mutation in a KIAA0586 ortholog (ENSGALG00000012025), a gene not previously attributed with any known function. We show a direct causal link between KIAA0586 and the mutant phenotype by rescue experiments. KIAA0586 encodes a novel protein, apparently specific to vertebrates, that localizes to the cytoplasm. We show that Gli3 processing is abnormal in talpid\textsuperscript{3} mutant cells but that Gli3 can still translocate to the nucleus. These results suggest that the talpid\textsuperscript{3} protein operates in the cytoplasm to regulate the activity of both Gli repressor and activator proteins.

\textbf{Keywords:} Gli; Hedgehog signaling; chicken; talpid\textsuperscript{3}

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[Gli3R]. This results in low levels of full-length Gli3 protein that, together with other Gli proteins, can act as a transcriptional activator [Gli3A] and a gradient of Gli3R, highest anteriorly [Wang et al. 2000]. Absence of high-level expression of some target genes in the posterior of talpid3 limb buds [e.g., Ptc1] and the inability to rescue their expression through the addition of Shh protein [Lewis et al. 1999a] suggests that GliA function is defective. Ectopic expression of other target genes in the anterior of talpid3 limb buds suggests that Gli3R levels are reduced anteriorly. The absence of high-level expression of Ptc, which encodes the Shh receptor and binds Shh, could lead to widespread diffusion of Shh ligand, reducing Gli3R levels. However, the limbs of Gli3−/− and Shh−/−, Gli3−/− mutant mice, like those of talpid3 chick embryos, are polydactylous, with many unpatterned digits, and also show ectopic expression of Hh target genes [Hui and Joyner 1993; Litingtung et al. 2002; te Welscher et al. 2002].

Here we show that ectopic gene expression in talpid3 limb buds is ligand independent and assess the distribution of Gli3A versus Gli3R. The dorsoventral pattern of the neural tube in chick has been shown to depend on a balance between GliA and GliR function (Persson et al. 2002; Stamataki et al. 2005). We explore whether the talpid3 mutation compromises both GliA and GliR function in dorsoventral patterning of the neural tube and adjacent somites. We rescue Gli function by electroporation into the talpid3 neural tube. We then combine knowledge of the chicken genome with the manipulability of chick embryos to identify the talpid3 gene and carry out functional complementation tests within the mutant neural tube to confirm identification unequivocally. We show that the talpid3 protein localizes to the cytoplasm and that although Gli3 processing is abnormal in mutant chick cells, both Gli3A and Gli3R can still translocate to the nucleus. We conclude that the talpid3 protein acts in the cytoplasm to regulate the functional activity of both the repressor and activator forms of Gli.

Results

Basis of the talpid3 limb polydactyly

The polydactylosus phenotype of talpid3 limbs suggests a gain of Hh function. Comparison of stage 19 Hamburger Hamilton [HH] (Hamburger and Hamilton 1951) limb buds using immunohistochemistry showed that Shh protein is more widespread in talpid3 [Fig. 1A,B]. In Western blots, more Shh protein was found in the middle third of talpid3 limb buds than in wild type [Fig. 1C]. To test whether ectopic gene expression in talpid3 limb buds is dependent on this ectopic Shh protein, we attempted to rescue the mutant phenotype by inhibiting Shh signaling or removing its source, we monitored rescue by examining Hoxd13 expression, which is ectopically expressed throughout talpid3 limb buds instead of being posteriorly restricted [Izpisua-Belmonte et al. 1992]. We applied cyclopamine, which inhibits Smo activity [Frank-Kamenetsky et al. 2002] to stage 17 HH wing buds. In 5/6 treated talpid3 wings, Hoxd13 expression was still strongly expressed [Fig. 1E; right wing bud] whereas, in 3/4 treated wild-type wings, expression was much reduced [Fig. 1D; right wing bud]. Expression of Hoxd13 was retained in most cases in wings treated with ethanol [4/5 wild-type, 3/3 talpid3] [data not shown]. We also removed future Shh expressing cells at stage 16 HH. This had no effect on Hoxd13 expression in talpid3 wing buds [3/3] [Fig. 1G, right wing bud] but, in wild type, expression was reduced or abolished [7/7] [Fig. 1F, right wing bud]. These results show that, although Shh protein is more widely distributed in talpid3 limb buds, ectopic Hoxd13 expression is ligand independent.

Analysis of gene expression in talpid3 limb buds and the fact that these changes in expression are ligand independent suggest that both GliA and GliR functions are defective. In order to assess the levels of the different forms of Gli proteins, we extracted proteins from the anterior, middle, and posterior thirds of talpid3 buds [either wing or leg] and carried out Western blot analysis using an antibody against Gli3 that recognizes both the full-length form, Gli3A [190 kDa] and the processed short form, Gli3R [83 kDa]. We then compared the levels of the two forms of Gli3 with those seen in wild-type limb buds by carrying out analysis on either wing buds or leg buds. We present the data in histograms for the wing buds and show the Western blot for the leg buds. In the wild-type limb buds, we detected both Gli3A and Gli3R forms [Fig. 1H,I] and, as previously reported [Wang et al. 2000], Gli3R is present in a gradient along the anterior–posterior axis with maximal levels of Gli3R in the anterior region of the bud [Fig. 1H,I]. In contrast, in talpid3 wing buds [Fig. 1H], levels of Gli3A are strikingly increased and the polarized distribution of Gli3R is abolished. Western blots of Gli3 in talpid3 leg buds [Fig. 1H] also confirmed that Gli3R is not graded and, in addition, that Gli3A levels are strikingly elevated. We also carried out Western blot analysis on extracts from whole limb buds [both wing and leg pooled together] from wild-type and talpid3 embryos and estimated the Gli3A/Gli3R ratio [Fig. 1]. This analysis shows that this ratio is strikingly elevated in the mutant. Furthermore, we found that the ratio of Gli3A/Gli3R was also elevated in extracts from talpid3 trunk, which includes other tissues, such as neural tube and somites, that are patterned by Hh signaling. Thus there is a generalized defect in Gli3 processing in talpid3 embryos that leads to high levels of activator compared with repressor.

Patterning of talpid3 neural tube and somite

Floor plate and associated Shh signaling is markedly reduced in talpid3 neural tube of stage 20 embryos. Shh transcripts and protein are expressed in talpid3 notochord, as in wild-type embryos, but are extremely patchy or completely absent in floor plate [Fig. 2, cf. A1,B1 and A2,B2]. In wild-type embryos, floor plate is also characterized by Shh-dependent HNF3β/FoxA2 expression [Fig. 2D1], which is either very reduced or absent in talpid3.
High-level expression of Ptc1 or Ptc2 genes, considered to be a direct readout of Shh signaling (Pearse et al. 2001), is lost in talpid3 embryos (Fig. 2, cf. C1 and C2; see Lewis et al. 1999a).

We characterized dorsoventral patterning of the neural tube in talpid3 embryos, investigating markers of chick neuronal identity that are established by Hh signaling, (Persson et al. 2002). We used embryos at stage 20 when the mutant phenotype is readily observable. Nkx2.2 (p3 progenitor cells) (Fig. 2E2) and Islet2 (MNv) (Fig. 2G2) is almost lost completely while expression of Islet1 (MN) [Fig. 2F2, arrow indicating residual expression] and Lim3 (MN and V2) [Fig. 2H2, arrow indicating residual expression] is either lost or expressed in only a few ventrally located midline cells. Expression of intermediate markers, Pax6 [Fig. 2I2] and Dbx2 [Fig. 2J2] extends into the ventral-most region of the neural tube, and Lim1/2-positive cells, normally located in a stereotypical pattern in the intermediate-dorsal region (Fig. 2I1), are found more ventrally and wild-type pattern is lost (Fig. 2K2). En1 expressing cells [V1] [Fig. 2L1, bracket] are also shifted ventrally and distributed more widely [Fig. 2L2, bracket]. Expression of dorsal markers Gsh1 and Pax7 is expanded ventrally (Fig. 2M2,N2) with Pax7, normally expressed in dorsal third (Fig. 2N1), being expressed in dorsal half of talpid3 neural tube (Fig. 2N2) and the band of Gsh1 expression being broader (Fig. 2O2, bracket).

In summary, in talpid3 there is a loss and/or reduction of ventral genes [talpid3, Fig. 2O, regions A and B] accompanied by ventral expansion of genes normally expressed in dorsal neural tube, suggesting a loss of Hedgehog function and failure of Gli activator. Expansion of intermediate neural [talpid3, Fig. 2O, region C] tube genes more ventrally suggests a loss of Gli repressor.

We examined dorsoventral patterning of somites, which is controlled by Shh from notochord and floor plate in the chick, mouse, and zebrafish (Munsterberg et al. 1995; Borycki et al. 1999; Lewis et al. 1999b). As in neural tube, there is low-level Ptc2 expression throughout talpid3 somites [Fig. 2C2, arrow]. In talpid3, Pax1 is expressed more widely than in wild type [Fig. 3A] and positive cells are found displaced dorsally between myotome and dermomyotome [Fig. 3B, arrow] instead of be-
ing clearly demarcated from myotome expressing MyoD. The dermomyotome expresses Pax3 (Fig. 3C) and double in situ hybridization showed that, in talpid3 rostral somites, epithelial cells in dermomyotome express MyoD (Fig. 3D, arrow). Expansion of MyoD into more dorsal regions can be mimicked by overexpression of Shh in wild-type somites (Fig. 3E, arrow). Thus expansion and shift of cell types into more dorsal domains in talpid3 somites seems to resemble a gain of Hh function. To establish whether the effects of the mutation are autonomous, undifferentiated somites taken from the tail region of a stage 20 HH talpid3 embryo were implanted into stage 10–12 HH wild-type hosts. Widespread expression of MyoD in talpid3-derived somites was still seen (Fig. 3F, arrow) even in a wild-type environment. This suggests that gain of function in somite, as in limb, is more likely due to a defect in Hh signaling in responding cells than to ectopic ligand.

Figure 2. Expression of Shh and Shh-dependent genes in the dorsoventral axis of the neural tube in stage 20 HH wild-type and talpid3 embryos. Shh expressed in notochord and floor plate in wild-type (A1) and in notochord but not ventral neural tube in talpid3 (A2). Shh protein in notochord and floor plate in wild type (B1) but only in talpid3 notochord (B2). Ptc2 expressed strongly around notochord and dorsal to floor plate in wild type (C1) but weakly in talpid3 neural tube and abnormally in somite (arrow, C2). HNF3β/FoxA2-positive cells in floor plate in wild type (D1); fewer HNF3β/FoxA2-positive cells indicate reduced floor plate in talpid3 (D2). Nkx2.2 expression in p3 progenitors in wild type (E1) and reduced or absent in talpid3 (E2). Islet1 expression in motorneurons in wild type (F1), reduced in talpid3, remaining positive cells shown by arrows (F2). Islet2 expression in ventral motorneurons in wild type (G1) and absent in talpid3 (G2). Lim3 expression in p2 and motorneurons in wild type (H1), reduced in talpid3 (arrow, H2). Pax6 expression in wild type (I1) and talpid3 (I2). Dbx2 expression in wild type (J1); ventrally expanded in talpid3 (J2). Lim1/2 expression in p1-d14 neurons in wild type (K1); ventralized in talpid3 (K2). En-1 expression in p1 neurons in wild type (L1); broader and ventralized [bracket] in talpid3 (L2). Stripe of Gsh1 expression [bracket] in wild type (M1); expanded ventrally in talpid3 (M2). Pax7 expression in wild type (N1), expanded ventrally in talpid3 (N2). |O| Summary of neuronal progenitor domains in neural tube of wild-type and talpid3 embryos. A–D represent areas of neural tube dependent on different Gli activities (Persson et al. 2002). Talpid3 embryos lack floor plate, motorneurons, and p3 and p2 neurons but have expanded p0-d14 domains.


**taldip** gene and Hedgehog signaling

Failure to produce ventral domains of progenitor neurons in **taldip** neural tube could be due to reduced Shh protein because there is no floor plate. We first tested this by implanting Shh-soaked beads or Shh-expressing cells into **taldip** neural tube and examining Islet1 expression. Twenty-four hours later, there was no rescue of Islet1 expression in **taldip** embryos [9/9] (Supplementary Fig. S6J2). Further experiments in **taldip** embryos showed that application of a Shh bead to the neural tube did not induce Nx2.2 or high-level Ptc1 expression or alter either Pax6 or Pax7 expression (Supplementary Fig. S6J2,K2,L2,M) as is seen in wild-type embryos treated with Shh [for details, see Fig. 7, below]. These data show that Shh ligand cannot rescue dorsoventral patterning of the **taldip** neural tube and that a reduction in floor plate does not account for loss of ventral neurons.

Inability to rescue neural tube patterning with Shh suggests that **taldip** cells cannot transduce the Shh signal and that GliA does not function properly. To test this hypothesis directly, we electroporated neural tubes of stage 20 HH **taldip** and wild-type embryos with an activated Gli construct that can constitutively translocate to the nucleus [pCAGGS-Gli3A(H)] [Stamataki et al. 2005] and monitored dorsoventral gene expression. Cell-by-cell analysis showed that Nx2.2 [Fig. 4E1,E2], Islet1 [Fig. 4F1,F2, arrows], and Lim3 expression [data not shown] was recovered in **taldip** embryos while expression of Lim1/2 [data not shown], Pax6 [Fig. 4G1,G2, arrows], and Pax7 [Fig. 4H1,H2, arrow] was reduced in cells expressing the pCAGGS-Gli3A(H) construct [2/2]. In wild-type embryos, ectopic expression of Nx2.2 [Fig. 4A1,A2, arrow], Islet1 [Fig. 4B1,B2, top arrow], and Lim3 [data not shown] was also induced and Pax6 [Fig. 4C1,C2, arrow] and Pax7 [Fig. 4D1,D2, arrow] expression reduced. Electroporation of control pCAGGS-eGFP into neural tube of either **taldip** or wild-type embryos produced no gene expression changes [data not shown]. These results demonstrate directly that supplying **taldip** cells with functional activated Gli rescues the defect.

**Figure 3.** Expression of Shh-dependent genes in somites of the stage 20 HH wild-type and **taldip** embryos. MyoD (black) and Pax1 (red) expression in wild-type [A] and **taldip** somites [B]; arrow indicates abnormal Pax1 localization. MyoD (black) and Pax3 (red) expression in wild-type [C] and **taldip** somites [D]; arrow indicates abnormal MyoD localization. [E] Wild-type embryo infected with pRCAS-Shh (right somite), showing ectopic MyoD expression. [F] **Taldip** somite (right) implanted in wild-type embryo, showing continued abnormal MyoD expression (arrow).

**Rescue of **taldip** neural tube pattern**

Genetic mapping and identification of **taldip**

Linkage analysis of 110 individual carriers mapped the TA3 locus close to markers ADL0298 and ADL0166 on chromosome 5. Mapping further markers refined the location to an interval containing COMO184-[5.1]-ADL0166-[7.3]-SIX4-[3.6]-DAAM1-[0.9]-TA3-[4.6]-OTX2-[8.3]-ADL0298-[0.0]-ROS0530-[2.8]-BMP4 [genetic distances between markers in centimorgans]. We constructed a detailed physical map of this region to define gene content and develop more markers [Fig. 5A]. Using these markers, the location of the **taldip** mutation was reduced to an interval encoding five genes: KCNK16-DACT1-ENS-GALG00000012025-TIMM9-ARID4A [Fig. 5B].

To look for sequence changes that might identify the **taldip** mutation we sequenced cDNA clones derived from wild-type and **taldip** embryos [Supplementary Table S1]. Sequence analysis of **taldip** cDNA revealed an insertion mutation of a single thymine residue (Fig. 5C); this frameshift mutation is terminated nine residues after the thymine insertion at a stop codon [Fig. 5C]; this frameshift mutation is predicted to produce a truncated protein of 366 amino acids compared with 1524 in wild type [Fig. 6A]. A multispecies comparison of **KIAA0586** orthologs [Supplementary Fig. S2] shows extensive homology across all 30 exons, and a number of highly conserved noncoding regions. The complete sequence of the chicken **KIAA0586** mRNA is shown in Supplementary Figure S3. The translation initiation codon at position 137 was selected as the most likely based on the longest open reading frame and homology with other vertebrate orthologs [Supplementary Fig. S4]. To detect **KIAA0586** orthologs in other species, we combined information from conservation of sequence and gene order [Supplementary Figs. S4, S5]. Complete conservation of gene order was found for **DAAM1-DACT1-KIAA0586-TIMM9-ARID4A** in all vertebrates examined. No homologs were detected in Ciona
intestinalis, Drosophila melanogaster, or Caenorhabditis elegans. Using Codonml [PAML 3.13] we were able to estimate the $K_a/K_s$ ratio for KIAA0586 ($\sim 0.28$), a measure of selection constraint [Yang and Nielsen 2000]. For comparison, the $K_a/K_s$ ratio for mammalian orthologous gene pairs [Rat Genome Sequencing Project Consortium 2004] was 0.09–0.11, most genes being under strong to moderate purifying selection. The $K_a/K_s$ ratio for KIAA0596 indicates that this protein has been under reduced purifying selection and/or increased positive selection. No specific functional domains were predicted in the peptide sequence. Most highly conserved are three globular domains, coiled-coil regions, and a central region, with as yet, no known structural features, and least conserved is the C-terminal region [Fig. 6A].

Expression of talpid$^3$ gene and protein and analysis of Gli3 translocation in mutant cells

KIAA0586 is ubiquitously expressed in wild-type embryos [stages 12–35 HH], consistent with the talpid$^3$ mutation affecting multiple tissues [Fig. 6B]. Using the program ProtComp, the KIAA0586 protein was predicted to be cytoplasmic. In order to determine cellular localization experimentally, we expressed either C-terminal-tagged KIAA0586-myc or N-terminal-tagged KIAA0586-
HA in limb bud cells from wild-type chick embryos or in the chicken DFI cell line and visualized cellular localization by immunofluorescence. In all cases, labeling was confined to the cytoplasm (Fig. 6D,E), suggesting the talpid3 protein is a cytoplasmic protein.

To further investigate the role of KIAA0586 in Hh signaling, we compared intracellular localization of Gli3 in wild-type and talpid3 mutant chick limb bud cells. In one set of experiments, we isolated cytoplasmic and nuclear fractions from wild-type and mutant cells and then carried out Western blot analysis as before (Fig. 6F). We assessed the effectiveness of the fractionation by detecting tubulin and found this to be confined to the cytoplasmic fraction [Fig. 6F]. Both full-length [190 kDa] and processed [83 kDa] Gli3 proteins were readily detected in nuclei isolated from wild-type chick limb bud cells but not in the cytoplasmic fraction. Both Gli3 forms were also detected in the nuclei of talpid3 cells, although full-length Gli3 could also be detected in the cytoplasm of mutant cells [Fig. 6F]. Furthermore when the ratio of Gli3A/Gli3R was compared, it is evident that talpid3 cells from limb and head have a much higher ratio of Gli3A/Gli3R in the nucleus [Fig. 6G] than wild-type cells. We also expressed pGli3-myc in wild-type and talpid3 chick limb bud cells and visualized localization using immunofluorescence [Fig. 6H]. Localization of Gli3-myc was rather variable but was seen in both nucleus and cytoplasm in both wild-type and talpid3 cells. These results reinforce the conclusion that the talpid3 protein is required for efficient processing of functional GliA and GliR but suggest that it is not required for nuclear translocation of these proteins.

Figure 5. Mapping and identification of the talpid3 mutation in KIAA0586 (ENSGALG00000012025). (A) Results of typing backcross progeny. Values at bottom of figure are number of progeny inheriting chromosome 5 haplotypes from F1 carrier parent. White squares indicate wild-type (N) allele; black squares indicate the talpid3 (TA3) allele. (B) Chromosomal organization of TA3 locus relative to known genes. The top part of figure shows locations of bacterial artificial chromosomes, together with BLAST results using full-length cDNA sequences isolated in this region and markers used in genetic analysis. (C) Sequence trace files showing frameshift mutation in TA3 compared with N alleles. Translation products of alleles are shown below DNA sequences; the effect of frameshift mutation (TA3 allele) is shown as an altered amino sequence with an in-frame stop codon; details of marker sequences are in Supplementary Table S2.

Rescue of talpid3 neural tube by KIAA0586

To confirm that KIAA0586 is the talpid3 gene, we carried out complementation tests. In the first set of experiments, we tested whether KIAA0586 could rescue ectopic induction of dorsoventral markers by Shh in neural tube of stage 17–18 HH (talpid3) embryos. Shh beads were inserted into the neural tube and a pCAGGS-KIAA0586 construct was coelectroporated with a pCAGGS-eGFP control plasmid and dorsoventral patterning examined after 24 h. As noted above, application of a Shh bead to a wild-type neural tube induces ectopic Nkx2.2 (Fig. 7A2, arrows), Islet1 (Fig. 7B2, arrows), shifts strong Pax6 expression dorsally (Fig. 7C2, arrow), induces Ptc1 throughout the neural tube, surrounding somites, and ectoderm [Fig. 7I] and reduces Pax7 expression ventrally (Fig. 7D2, arrow) while application of Shh to a talpid3 neural tube has no effect on Nkx2.2, Islet1, Pax6, or Pax7 and only weakly induces Ptc1 [Supplementary Fig. 6I2,J2, K2,L2,M]. When wild-type tissue was electroporated with pCAGGS-KIAA0586 and treated with Shh, a change in gene expression of Nkx2.2, Islet1, Pax6, Pax7, or Ptc1 was observed on both sides of the neural tube, whether electroporated or not, and therefore attributable only to the effect of the Shh bead [Fig. 7A–D]. However,
when talpid<sup>3</sup> embryos were provided with both Shh and KIAA0586, ectopic expression of Nkx2.2 was induced only on the electroporated side of the neural tube (2/2) [Fig. 7E1–E3, arrows] and sense probe (right) RNA probes. Expression of KIAA0586 in stage 20 HH chicken embryos, using antisense probe (left) and sense probe (right). Application of Shh with KIAA0586 also induced high-level Ptc1 expression in talpid<sup>3</sup> dorsal neural tube on the electroporated side (Fig. 7J; asterisk denotes electroporated side). In preliminary experiments, one talpid<sup>3</sup> embryo had a reduction in Pax7 when electroporated with pCAGGS-KIAA0586 (1/1) (Supplementary Fig. S6H1,H2) but Nkx2.2, Islet1, and Pax6 remained unchanged (Supplementary Fig. S6E–G), and there was no effect on expression of Nkx2.2, Islet1, Pax6, or Pax7 in a wild-type embryo electroporated with pCAGGS-KIAA0586 at stage 17 HH (1/1) (Supplementary Fig. S6A–D).

In a second set of experiments, we tested whether KIAA0586 alone could rescue endogenous dorsoventral patterning of the neural tube in very early talpid<sup>3</sup> embryos. In order to carry out these experiments, we had to electroporate batches of embryos from the talpid<sup>3</sup> flock at stages 12–14, well before the mutant phenotype is observable. We electroporated the pCAGGS-KIAA0586 construct, together with pCAGGS-RFP and fixed embryos at stage 20HH in order to examine gene expression. At this stage, we could usually identify mutant embryos by their phenotype, and we confirmed their identity by genotyping. In talpid<sup>3</sup> embryos, we found very striking induction of Islet1 expression (3/3) (Fig. 7K1/2, green cells) coupled with repression of Pax6 (2/2) (Fig. 7L1/2, arrow). We also have preliminary evidence that Pax7 expression was reduced (1/1) (data not shown). This rescue of endogenous target gene expression provides good evidence that KIAA0586 is the talpid<sup>3</sup> gene and has an essential role in Hh signal transduction.

Discussion

Hh signaling plays crucial roles in development and disease, and therefore it is important to understand the signal transduction pathway that mediates Hh signaling. Here we identify a novel component of the signaling pathway in vertebrates and provide evidence that it is necessary for the function of both Gli repressor and Gli activator forms. By a positional cloning strategy, exploiting the recently assembled chick genome, we provide evidence that KIAA0586 is the talpid<sup>3</sup> gene and has an essential role in Hh signal transduction.
Moreover, a frameshift mutation in KIAA0586 is present in talpid3 mutants, and the expression of a wild-type KIAA0586 cDNA in the neural tube of talpid3 embryos rescued the Shh responsiveness of neural cells and endogenous dorsoventral patterning. We therefore propose that KIAA0586 be renamed Talpid3.

Our analysis of Hh target gene expression in limb, face, neural tube, and somite of talpid3 embryos, together with our findings that expression of target genes is ligand independent—insensitive to either presence or absence of Shh—and can be rescued by expressing activated Gli—are consistent with the idea that both GliA and GliR functions are compromised in talpid3. Thus the Talpid3 gene product plays an essential role in both GliA and GliR function in the Hh pathway. The paradoxical talpid3 phenotype, an apparent mixture of gain and loss of Hh function, is explained by the fact that GliR plays a predominant role in limb and somite, whereas GliA function is more important in face and neural tube patterning.

Our data show that Gli3 processing is impaired in talpid3 mutant cells, leading to the presence of both full-length Gli3A and Gli3R. Levels of Gli3A, in particular, are markedly increased. Although changes in processing are likely to be the main cause, changes in protein longevity and transcriptional levels could also contribute. The net result is that the ratio of Gli3A/Gli3R is much greater in talpid3 mutant cells. Abnormal processing is found not only in cells from the limb but also in cells from the face and neural tube.
from the trunk, which includes neural tube and somite. We have also shown that, as predicted by its structure, Talpid3 protein is localized in the cytoplasm. Thus, our results are consistent with Talpid3 interacting with other members of the Hh signaling complex to regulate processing of Gli proteins in the cytoplasm. Given the high levels of full-length Gli3, it is not clear why GliA function, in addition to GliR function, is compromised in talpid3. This is even more puzzling since we have also shown that the absence of Talpid3 protein does not prevent the ability of Gli3 proteins including Gli3 activator to enter the nucleus. The most likely possibility is that the pathway is very sensitive to the precise levels of full-length and short forms of Gli proteins such that, in the talpid3 mutant, the levels of GliA and GliR counterbalance their effects, resulting in neither activation nor repression. Alternatively, the Gli3 proteins produced in the absence of Talpid3 may be unable to regulate transcription due to, as yet, unknown post-translational modifications.

Recently two other genes involved in Hh signaling, Dzip1 (Sekimizu et al. 2004, Wolff et al. 2004) [chicken ortholog ENSGALG00000016895] and MTSS1 (Callahan et al. 2004) [also called MIM/BEG4, chicken ortholog ENSGALG00000016333], have been described. Dzip1 was identified as the Zebrafish mutant gene in the iguana mutant, which shows many similarities to the talpid3 mutant, including reduction of expression of Shh-dependent genes in neural tube coupled with a gain of Hh signaling in the somite. Furthermore, as in talpid3, iguana cannot be rescued through manipulation of Shh ligand, leading to the suggestion that either both GliA and GliR functions are reduced [Sekimizu et al. 2004], similar to our proposal for talpid3, or that GliR fails because of constitutive low-level Gli1 activation (Wolff et al. 2004). There is evidence that Dzip1 can shuttle between cytoplasm and nucleus, and it has been suggested that Dzip1 may affect nuclear import of Hh pathway proteins. This contrasts with Talpid3, which appears to be confined to the cytoplasm and is not required for nuclear import of Gli3. Interestingly, constitutive activation of Shh signaling has been suggested to occur in the talpid3 chicken mutant (Chuang and McMahon 1999), in which high levels of Gli3A are also found [Wang et al. 2000]. Talpid3, like talpid3, is polydactylous, and the many digits are unpatterned, but, unlike talpid3, there is high-level Ptc expression throughout the limb (Carrucio et al. 1999), suggesting that Gli activator is functional in this mutant. Thus similarities in phenotype could arise by quite different mechanisms.

A number of intraflagellar transport proteins have been shown to play an essential role in vertebrate Hh signal transduction (Huangfu et al. 2003) in mouse, and a recent report suggests a functional link between Hh signaling and cilia at the level of the transmembrane protein smoothened which is required for GliA function (Corbit et al. 2005). Analysis of hypomorphic mouse mutants of two intraflagellar transport proteins reveals striking parallels between these mutants and talpid3 (Liu et al. 2005). Not only are the alterations in gene expression patterns in limb and neural tube similar to those seen in talpid3 and insensitive to Hh ligand, but also high levels of full-length Gli3 were detected in mutant cells, giving rise to a marked increase in the Gli3A/Gli3R ratio. Like Talpid3, intraflagellar transport proteins appear to be required for both GliA and GliR functions. It will be important to determine why mutations in intraflagellar transport proteins compromise GliR function in addition to GliA function and to explore the relationship between Talpid3 and cilia. Talpid3 joins a growing list of proteins, including these intraflagellar transport proteins, that regulate Hh transduction specifically in vertebrates (Chuang and McMahon 1999, Eggenschwiler et al. 2001) and is the first component in this pathway to be discovered in chickens.

Materials and methods

Embryo manipulations

Eggs were incubated for 2.5 d at 38°C, then windowed to assess development and classified as either mutant or wild type and reincubated until the desired stage. All limb manipulations were carried out on the right wing, leaving the left wing as a control.

Cyclopamine treatment: One-hundred microliters of 5 mM cyclopamine in 95% EtOH diluted with 200 µL DMEM was sonicated for 10 min; for the control solution, 100 µL of 95% EtOH was diluted in 200 µL DMEM. Solutions were injected with a fine glass micropipette into the amniotic sac over the right wing of stage 20 HH embryos; eggs were reincubated for 24 h.

Removal of Shh-expressing cells: At stage 16 HH, tissue was removed from flank, immediately lateral to somites, from axial level somites 22 and 18/17 using a sharpened tungsten needle; eggs were then reincubated for 18 h.

RCAS virus production, microinjection, and somite grafts

RCAS virus production and microinjection were done as per Morgan and Fekete (1996). In ovo surgical experiments were performed as per Schmidt et al. (2000), and eggs were reincubated for 40 h.

Tissue graft implants—neural tube

QT-6 Shh expressing cells were grown until confluent. Cell sheets were scraped from the dish surface. A small piece of sheet was folded and tucked into a slit made in the neural tube at the level of the hind limbs using a tungsten needle; eggs were then reincubated for 24 h.

Bead implants—neural tube

CM Affi-Gel Blue Beads (Bio-Rad) soaked in Shh protein as per Drossopoulou et al. (2000) were picked up on the point of a sharpened tungsten needle and placed into the neural tube via a dorsal slit.

Electroporation

DNA was prepared using a Qiagen Endotoxin-Free Maxiprep Kit, resuspended in endotoxin-free water, and diluted with 0.25% Fast Green. Plasmid pCAGGS-Gli3AEG-Ch was used at a
concentration of 7 µg/µL, pCAGGS-GFP at 7.5 µg/µL, pCAGGS-RFP at 0.1 µg/µL, and pCAGGS-KIAA0586 at 1 µg/µL.

DNA was injected into the neural tube and embryos were immediately electroporated at 30 V for 5 × 50 msec with 5 × 50-100-msec intervals or at 20 V for 5 × 15 msec [stages 12-14]. Embryos were reincubated for 20-48 h. Successful electroporation was assessed by expression of GFP, eGFP, or RFP using a Leica Fluorescence Dissection Microscope. The GFP section of neural tube was then dissected out in cold PBS (pH 7.4) and fixed for sectioning for immunohistochemistry or whole-mount in situ hybridization.

Whole-mount RNA in situ hybridization
For details, see the Supplemental Material.

Whole-mount immunohistochemistry
For details, see the Supplemental Material.

Section immunohistochemistry
For details, see the Supplemental Material.

Western blotting
For determining levels of Shh protein, stage 20 HH embryo limb buds were dissected into three equal parts along the anterior-posterior axis in cold PBS, lysed in RIPA buffer/1:125 Proteases Inhibitor (Roche), samples ran on 12% SDS-PAGE, and protein detected with Shh antibody. Lysates were spun at 13,000 rpm for 5 min at room temperature, supernatant was removed and methanol precipitated and then dried using the Eppendorf Concentrator. The pellet was resuspended in 30 µL of Sample Buffer 1/10 β-mercaptoethanol and then denatured. Gels were subsequently wet or dry blotted in 1× Tris-Glycine/20% Methanol buffer for 1–2 h at 172 mA onto nitro-cellulose, which was blocked in 5% Marvel/PBS 1:1000 Tween-20; incubated with 1:2 antibody and Marvel/PBT overnight at 4°C, washed 3 h in PBT; incubated in anti-mouse HRP-conjugated (Sigma) in Marvel/PBT 1:2 antibody and Marvel/PBS 1:100 Tween-20; incubated with 1:2 antibody and Marvel/PBT overnight at 4°C, washed 3 h in PBT; incubated in anti-mouse IgG conjugated with Alexa Fluor 610 (1:1000, Molecular Probes) for 1 h at room temperature. After washes (3 × 5 min in 0.2% Tween-20 in PBS, and incubated in anti-mouse IgG conjugated with Alexa Fluor 610 (1:1000, Molecular Probes) for 1 h at room temperature. After washes (3 × 5 min in 0.2% Tween-20 in PBS), cells were incubated in VectaShield Hard’set mount medium with DAPI ([Vector Laboratories, H-1500]). Fluorescence was observed using a fluorescence microscope or a Leica SP2 confocal microscope.

Animals and genetic linkage analysis
Talpid3 carriers were maintained by outcrossing with ISA Brown chickens. Line 6, an inbred White Leghorn line, was kindly provided by the Institute of Animal Health (Compton). A male carrier (TA3/N) was crossed to eight Line 6 females (N/N) and offspring of this backcross were test-crossed with known carriers. A carrier was confirmed if two or more talpid3 embryos were found from a test cross. At least 20 wild-type embryos were collected before any noncarriers were confirmed. Four DNA pools were created from backcross offspring: Carrier male (n = 13), carrier female (n = 32), noncarrier male (n = 7), and noncarrier female (n = 16) were genotyped using 129 autosomal genetic markers, covering 70% of the genome. Markers ADL0298 and ADL0166 on chromosome 5 showed a significant difference (p < 0.00001) between carrier and noncarrier pools. Further markers near these loci were used to genotype 110 individuals and refine the location of the TA3 locus. Two-point and multipoint linkage analysis was performed using CRIMAP (Green et al. 1990). From this analysis, 30 recombinant offspring were identified near TA3 between markers ADL0166 and ADL0298 and typed using markers developed from EST and genomic sequences. Using known chicken genes and reference to the Ensembl [http://www.ensembl.org] and University of California at Santa Cruz [http://www.genome.ucsc.edu] genome browsers, we identified the orthologous region on human chromosome 14. Using human gene sequences and Blast we searched databases [http://www.ncbi.nlm.nih.gov] for homologous chicken EST and genomic sequences. We developed PCR-based markers from these showing size and SSCP or SNP variation. These markers were used to isolate and order individual BAC clones (Burt et al. 2003) to create a detailed physical map. BAC-end and full-length cDNA sequences were also used to create more genetic markers. Using such a high density of markers we were able to identify specific haplotypes from recombinants in this region and map the TA3 locus to KCNK16-DACT1-KIAA0586-TIMM9-ARID4A. Genotyping was performed as described by Burt et al. [2003] and primers used for genotyping are listed in Supplementary Table S2.
Sequence analysis and characterization of talpid3 mutation
For details, see the Supplemental Material.

Genotyping
Genomic DNA was prepared from extra-embryonic membranes using Quigen DNAeasy Kit. A 957-base-pair [bp] region of the talpid3 gene was then amplified via PCR (forward: CTTCTCT TGCCCTTGCTTAC; reverse: TTGAAGCTGATTTCACA CAG), annealed at 60°C (Thermo electron) using Fast Start Taq Polymerase and GC-rich solution [Roche]. The PCR product was then digested using Pst1 [Roche]. A single 957-bp band indicates a wild-type embryo, two bands [721 bp and 236 bp] indicate a talpid3 mutant, and three bands indicate a heterozygous embryo.

Cloning of chicken cDNA clones and gene constructs
RNA was extracted using TRIzol reagent [Invitrogen], and a DACT1 cDNA was cloned via RT–PCR [P1: GGATGCTG GCCTATTTAAC; P2: GCTTCCCAAAG CAGAAACAG, in 3′ UTR] from embryo-derived mRNA (HH stage 21) using the TOPO TA cloning kit [Invitrogen], then subcloned into pGEM [Invitrogen] for preparation of antisense RNA probes. Rapid amplification of 5′ cDNA ends of KIAA0586 and DAAM1 was carried out using the First Choice RLM-RACE Kit [Ambion] and cloned using the TOPO TA cloning kit. Gene-specific primers are listed in Supplementary Table S2.

Bioinformatics analyses
For details, see the Supplemental Material.

Accession numbers
All sequences have been deposited in GenBank under accession numbers DQ066927–DQ066935 and CZ550237–CZ550250.

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